Fr m: Sent: Bunner, Bridget

Friday Avayot

I : Subject: Friday, August 02, 2002 4:31 PM STIC-Biotech/ChemLib

sequence search

10/10/2000

Hi! I'd like to request a sequence search for case 09/686,020:

1. the amino acid sequence of SEQ ID NO: 2

10/12/1999

Thanks!

Bridget Bunner

Art Unit 1647 CM1-10D12 (703) 305-7148 mailbox 10B19

Mark consider maring 103 12-1

Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 703-308-3534 AUG -2 2863

(22) 1 (C.S.)

Searcher:
Phone:
Location:
Date Picked Up: 8/6,
Date Completed: る/ つ
Searcher Prep/Review:/
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:/
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):
Questel/Orbit: DRLink: Lexis/Nexis: Sequence Sys.: WWW/Internet:

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Sequence Seq Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence 48, 1 Sequence 4, Ar Sequence 6, Ap Appli Appli Appli Appli Appli Appli Appli Appli

> Sequence 1 Sequence 8 Sequence 8 Sequence 6 Sequence 6

Sequence

us-09-686-020a-2.rai

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APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa
APPLICANT: Warty, Lynn E.
APPLICANT: Warty, Lynn E.
APPLICANT: Warty, Seete
ITILE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                           US-09-116-498-4
US-09-116-498-6
US-09-275-3848-5
US-09-116-498-2
US-09-116-498-2
US-09-875-373-20
US-09-232-878-2
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-045-583-55
US-07-759-568-1
US-08-450-393A-8
US-08-390-000A-5
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SOFWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                         US-09-178-637-2
US-09-045-583-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-00476-8
US-08-202-056-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM:
COMPUTER: DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-446-669-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGBAT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-0166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08966316
Patent No. 5932445
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIMBELATE: UTRSNOT11
CLONE: 2547002
US-08-966-316-16
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(without alignments)
653.091 Million cell updates/sec
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Sequence 19,
Sequence 19,
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Sequence 19,
Sequence 15,
                                                                                                                                                                                                                                                                        August 6, 2002, 18:04:30; Search time 13.09 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-966-316-18
US-08-153-848-19
US-09-108-3378-19
US-09-088-3378-19
US-09-29-843A-15
US-09-29-843A-15
US-09-251-545-1
US-09-29-843A-7
US-09-088-3378-7
US-09-088-3378-7
US-09-088-3378-7
US-09-088-3378-7
US-09-088-3378-2
US-08-383-751A-2
US-08-383-751A-2
US-08-383-751A-2
US-09-266-464-2
US-09-266-464-2
US-09-153-848-24
US-09-266-464-2
US-09-153-848-24
US-09-153-848-24
US-09-153-848-24
US-09-153-848-24
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1819
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                               181 NARCIPIEPRYLGTSMKALIQMLEICIGEVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Godska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell,
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                    ;
0
                                                                                                                                                Length 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
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                                                                                                                                            89.1%; Score 1620; DB 2;
86.0%; Pred. No. 7.1e-131;
iive 27; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR PAPLICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/POCKET UNBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/153,84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                              Query Match
Best Local Similarity 86.0
Matches 301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606
COMPUTER READABLE FORM:
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Bickne STREET: 6300 Sear CITY: Chicago STATE: Illinois
                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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RESULT 5
US-09-088-337B-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 DLORSSSEQAMRCSLITEH --- VEAFITIOVA ONVIGEL VPLLAMSFCYLVIIRTLLOAR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD 337
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                          1 MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
                                                                                                                                                                                                                                                                            APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           38;
                                                                                                                                                                                         Length 358;
                                                                                                                                                                                      36.2%; Score 659; DB 1; Length 358; 38.7%; Pred. No. 6.7e-49; Live 66; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 1111nois
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APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-299-843A-19
: Sequence 19, Application US/09299843A
: Patent No. 6107475
: GENERAL INFORMATION:
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
                                                                                                                                                                                    Query Match
Best Local Similarity 38.7%
Matches 144; Conservative
                                                                                                                   ; MOLECULE TYPE: protein US-08-153-848-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 SEGPTEPTSTFS 349
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                                                                                                   TOPOLOGY: linear
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121 LNFVSGMQFLACISIDRYVAVTKVPS----QSGVGKPCWIICFCVWMAAILLSIPQLVFY 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray, Patrick W. Schwelkart, Vicki L. Schwelkart, Vicki L. TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.2%; Score 659; DB 3; Length 350
38.7%; Pred. No. 6.7e-49;
.1ve 66; Mismatches 124; Indels
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                                                                                                                                                                                         NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/POCKET NUMBER: 27866/32059B
TELECOMMUTCATION INFORMATION:
TELEPHONE: (312) 474-6300
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/09088337B
Patent No. 6348574
GENERAL IRFORMATION:
APPLICANT: Godiska, Ronald
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SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
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STATE: Illinois
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Best Local Similarity
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----AETTTTES 357
                                                                                                         CITY: Chicago
STATE: Illinois
                                                                                                                                                              90909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66; Mismatches 124; Indels
                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.2%; Score 659; DB 4; 38.7%; Pred. No. 6.7e-49;
                                                                                                                PRIOR DATE: 01-Jun-1998
CLASSIFICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION STATE
PRIOR APPLICATION STATE
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 35,302
ATTORNEY/AGRAT INFORMATION:
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31,304
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONES: (312) 474-6300
TELECHONES: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-09-088-3378-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 358 amino acids TYPE: amino acid
                                                                                                    CURRENT APPLICATION DATA:
ZIP: 60606
COMPUTER READABLE FORM:
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Best Local Similarity 38.79
Matches 144; Conservative
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PCT-US93-11153-19
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61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLEFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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Best Local Similarity 38.7%; Pred. No. 6.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps
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TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MC-COMPANYANCE OF COMPUTED THE COM
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TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Noland, Greta E. REGISTRATION NUMBER: 3
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; MOLECULE TYPE: protein
PCT-US93-11153-19
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61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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315 ACVRCCVNPFLYAFIGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVE---- 369
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Godiska, Ronald
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Patrick W.
APPLICANT: SCHWEIkart, Vicki L.
TITLE OF INVENTION: NO. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE MADPRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.2%; Score 659; DB 3; Length 378; 38.7%; Pred. No. 7.1e-49; ive 66; Mismatches 124; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UN-1998
PRIOR APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09299843A Patent No. 6107475 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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Best Local Similarity 38.7%
Matches 144; Conservative
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MOLECULE TYPE: protein
US-09-299-843A-15
                                                                338 SEGPTEPTSTFS 349
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                                                                                                                      GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Partick with the structure of the structure
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STATE: 111inois
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804 and Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
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TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
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ADDRESSEE: Marshall, O'Toole,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
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Best Local Similarity 38.78
Matches 144; Conservative
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TOPOLOGY: linear
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STATE: Illinois
COUNTRY: USA
   SEGPTEPTSTFS 349
                                                            ----AETTTTES 377
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Fatent No. 6153441

GENERAL INFORMATION:

APPLICANT: Edward R. Appelbaum

APPLICANT: Dohn R. White

TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND

TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION THEREOF

FILE REPERENCE: P90753

CURRENT APPLICATION NUMBER: US/09/251,545

CURRENT APPLICATION NUMBER: 60/074,883

EARLIER FILING DATE: 1999-02-17

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FASTER FOR NOW ON VERSION 3.0
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                                                                                          TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP
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38.7%; Pred. No. 7.1e-49;
ive 66; Mismatches 124; Indels
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61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEFSGMELELCISIDRYVAIVQAVSAHRHRARVELISKESCVGIMILATVESIPELLYS 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INFUTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: = --=:= :: :=
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38.7%; Pred. No. 7.1e-49;
Live 66; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                          Gerstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <UNKNOWN>
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SEQUENCE DESCRIPTION: SEQ ID NO: 15:

92-09-088-3378-15
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121 LNFVSGMOFLACISIDRYVAVTKVPS----QSGVGKPCWIICFCVWMAAILLSIPQLVFY 176
                        292 ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD 337
                                                                                                                                                                                                                                                                TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP 231
                                                                                                                                                          NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
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Pred. No. 7.8e-49;
; Mismatches 124;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY AGENT INFORMATION:
NAME: NO. 5759804and, Greta E.
REGISTATION NUMBER: 35,3102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
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38.7%; Pred
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR EQUID NO: 7:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 38.7%
Matches 144; Conservative
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----AETTTTFS 377
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                 292 ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD 337
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                                                           232 NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI
                                                                                                                                         38;
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Best Local Similarity 38.7%; Pred. No. 7.1e-49;
Matches 144; Conservative 66; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                              Sequence 15, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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amino acid
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; MOLECULE TYPE: protein
PCT-US93-11153-15
                                                                                                                                                                                               338 SEGPTEPTSTFS 349
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COUNTRY: USA
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MVVAIVAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
                                                          121 LNFVSGMQFLACISIDRYVAVTKVPS----QSGVGKPCWIICFCVWMAAILLSIPQLVFY 176
                                                                                                                 177 TVNDNA-----RCIPIFPRYLGISMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP 231
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                                                                                                                                                                                                                                                                     292 ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD 337
                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS: 66
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Andresere.
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COUNTRY: USA
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ER: 27866/32059B
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PRIOR APPLICATION DATA:
APPLICATION UNBER: US 09/088,337
FILING DATE: 01-UNN-1998
FRIOR APPLICATION UNBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION UNBER: US 07/977,452
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (312) 474-0448
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
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----AETTTTFS 409
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Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 ALFHSCLNPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQRQSVEEFPFD
                                                                                                                                                               Length 410;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
                                                                                                                                                       ; Score 659; DB 3; L; Pred. No. 7.8e-49; 66; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Godiska, Ronald
                                                                                                                                                       36.2%;
Best Local Similarity 38.7%;
Matches 144; Conservative 66
                       : 410 amino acids amino acid
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acic
                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
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Search completed: August 6, 2002, 18:08:28 Job time: 238 sec
                       APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      NAME: NO. Land, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELESX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 38.7%
Matches 144; Conservative
        CURRENT APPLICATION DATA:
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GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
COMMESPONDENCE ADDRESS:
ADDRESSEE: BICKNell
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
ATTORNEY/AGENT INFORMATION:

NAME: NO. 6448574and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELEPHONE: (312) 474-6300

TELEPHONE: (312) 474-6448

TELEX: 25-3856

INFORMATION FOR SEO ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 410 mmino acids
                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-088-3378-7
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 38.79
Matches 144; Conservative
                                                                                                                                                                                           TYPE: amino acid
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402 ----AETITIFS 409
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                                                                            1 MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
                                                                                                                                                                                                                                                             TVNDNA-----RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMP
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                                       38;
  Length 410;
                                       Indels
36.2%; Score 659; DB 5; L
38.7%; Pred. No. 7.8e-49;
iive 66; Mismatches 124;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                              OM protein - protein search, using sw model
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August 6, 2002, 18:07:30 ; Search time 13.42 Seconds (without alignments) 1009.824 Million cell updates/sec Run on:

US-09-686-020A-2 1819 1 MALEQNQSTDYYXEENEMNG.....VEEFPFDSEGPTEPTST 350 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Document of		Q9npb9 homo sapien	bos t	P32248 homo sapien	P47774 mus musculu	O9wut7 mus musculu	P51686 homo sapien	mas m	_	cerco	_	macac	homo	) homo	homo	pan t	ğ	P35411 rattus norv		-		_	Q28519 macaca mula	Q9j121 mus musculu	097571 canis famil	Q9z0d9 mus musculu	P35344 oryctolagus	_	P21109 oryctolagus	9z2i3 cavia	3099	5930 bos t	28003 bos ta	P56491 papio anubi
SUMMARIES	£	1		CKRB_BOVIN	CKR7_HUMAN	CKR7_MOUSE	CKR9_MOUSE	CKR9_HUMAN	CKR6_MOUSE	CKR6_HUMAN	CCR6_CERAE	CCR6_MACMU	CCR6_MACNE	CCR6_HUMAN	CKR4_HUMAN	IL8B_HUMAN	IL8B_PANTR	CKRA_HUMAN	C3X1_RAT	CKD6_HUMAN	IL8B_GORGO	C3X1_HUMAN	CKR4_MOUSE	IL8B_MACMU	CKRA_MOUSE	IL8B_CANFA	C3X1_MOUSE	IL8B_RABIT	CKR2_MACMU	IL8A_RABIT	CKR3_CAVPO	CCR4_HUMAN	CCR4_BOVIN	1	CCR4_PAPAN
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062743 cercocebus P56498 felis silve	P55919 gorilla gor P56493 cercopithec O62747 cercocebus	Q28474 macaca fasc P79394 macaca mula	O54814 rattus norv P35407 rattus norv P56441 papio hamad	097880 pygathrix b P79436 macaca mula
CKR5_CERTO CCR4_FELCA	IL8A_GORGO CKR5_CERAE CCR4_CERTO	CCR4_MACMU	CKR3_RAT IL8B_RAT CKR5_PAPHA	CKR5_PYGBI CKR5_MACMU
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## ALIGNMENTS

RESULT 11  CKRB_HUMAN  TO CKRB_HUMAN  TO CKRB_HUMAN  TO GONEDS.  T
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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GCRDb; GCR_0757; -.
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350 AA;
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TRANSMEM
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                      NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
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Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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CKRB_BONIN STANDARD; PRT; 350 AA.

DCKRB_BOVIN STANDARD; PRT; 350 AA.

AC P35350;
DT 01-JUN-1994 (Rel. 29, Carated)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 16-OCT-201 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 11 (C-C CKR-11) (CCR-11)
DE (Possible gustatory receptor type B) (PPR1 protein).
                                                                                                                                                                                        N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                            100.0%; Score 1819; DB 1; Length 350; 100.0%; Pred. No. 1.3e-104;
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                                           G-protein coupled receptor; Transmembrane; Glycoprotein. DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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8E26049D2D5757C8 CRC64;
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CYTOPLASMIC (POTENTIAL).
                                                                        CYTOPLASMIC (POTENTIAL).
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        Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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InterPro; IPR000276; GPCR_Rhodpsn.
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350 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50263; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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PROSITE; PS00237;
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P47774;
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TRANSMEM
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TRANSMEM
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CONFLICT
SEQUENCE
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TRANSMEM
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                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                           01-0CT-1993 (Rel. 27, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
C_C chemokine receptor type 7 precursor (C-C CKR-7) (CC-CKR-7) (CKR-7) (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR OF RBW EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS. SUBCELLULAR LOCATION: INLEGEN MEMBRANE PICTELIO.
TISSUE SPECIFICITY: EXPRESSED IN WALLOUS LYMPHOID TISSUES AND ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Placenta;
MEDLINE-95154835; PubMed-7851893;
Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
Schwes T.B., Gray P.W.;
"Cloning of human and mouse EBII, a lymphoid-specific
G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
Genomics 23:643-650(1994).
          VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNP 300
                       -1- INDUCTION: BY EBV.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH HERPESVIRUS 6 OR 7. INDUCTION: BY EBV.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-93188173; Pubmed-8383238;
Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
                                                                                                                                                                                                                                                                                                                                                                           "Epstein Barr virus-induced genes: first lymphocyte-specific protein-coupled peptide receptors."; J. Virol. 67:2209-2220(1993).
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                378 AA
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EMBL; L31584; AAA74230.1; --
EMBL; L31582; AAA74230.1; --
EMBL; L31583; AAA74230.1; JOINED.
EMBL; L31581; AAA74230.1; JOINED.
EMBL; L31581; AAA74231.1; --
EMBL; L31581; AAA74231.1; --
EMBL; L31581; AAA74231.1; --
EMBL; A45680; A45680.
                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                CCR7 OR CMKBR7 OR EBI1 OR EVI1 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                               CKR7_HUMAN P32248;
                                                                                                                                                                                                                                                                                                                                                                  Kieff E.;
          241
                                                                                                                                   CKR7_HUMAN
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01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 7 precursor (C-C CKR-7) (CCR-7) (CCR-7) (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 VCLCQDEVIDDYIGDNT---TVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNG 77
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLONAC. . .) (POTENTIAL).
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                                                                                                                                                                                      C-C CHEMOKINE RECEPTOR TYPE
                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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L -> I (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 (POTENTIAL).
CYTOPLASMIC (F
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                                                                                                                                                POTENTIAL.
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CCR7 OR CMKBR7 OR EBI1 OR EBI1H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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337
378 AA;
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Best Local Similarity
                                                ROSITE; PS50262; protein coupled
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8
                                        65 IYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGMQFLACISIDRYVAVTKVPSQSG-----VGKPCWIICFCVWMAAILLSIPQLVFYT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 VNDNA----RCIPIFPRYLGTSMKAL--IQMLEICIGFVVPFLIMGVCYFITARTLMKM 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 QNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFITIVFVIGLAGNSMVVA 64
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InterPro; IPR000276; GPCR_Rhodpsn.
Ffam; PF00001; 7tm_1; 1.
PROSTE; PF00027; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN_RECEP_F1_2; 1.
I protein coupled receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL
DOWNENTAL
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
C-C CHEMOKINE RECEPTOR TYPE 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.7%; Score 650; DB 1; Length 378; 38.3%; Pred. No. 2.6e-33;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (1
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                                SEQUENCE FROM N.A.
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               Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.; "Cutting edge: identification of the orphan chemokine receptor GPR-9-6 as CCR9, the receptor for the chemokine TECK."; Immunol. 162:5671-5675(1999).
231 PNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTES 290
                                                                         FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
                                                         IALFHSCLNPILYVFMGASFKNYVMKVAKKYGSWRRQR-----QSVEFFPFDSEGPTE
                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN LYMPH NODES AND SPLEEN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 9 (C-C CKR-9) (CCR-9)
(Chemokine C-C receptor 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO1531; CHEMOKINER9.
PRINTS; PRO0237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 49
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR004069; Chemokine9_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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CYTOPLASMIC (
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MEDLINE=99248139; PubMed=10229797;
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                                                                                                                                                                                                                          STANDARD;
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                                                                                                                   344 PTSTFS 349
                                                                                                                                              372 TTTTFS 377
                                                                                                                                                                                                                                                                                                                            CCR9 OR CMKBR10.
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CKR9_MOUSE
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357 AA;
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MIM; 604738; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
MEDLINE-99248139; PubMed=10229797;
MEDLINE-99248139; PubMed=10229797;
Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
Cutting edge: identification of the orphan chemokine receptor GPR-9-6
as CCR9, the receptor for the chemokine TECK.";
J. Immunol. 162:5671-5675(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                     67 AYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : :| ||:::||||:||| | ||||||: | ||: |||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: 
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VSGESGIATCTMYYPKDKNAKLKSAVLILKVTLGFFLPFMVMAFCYTIIIHTLVQAKKSS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MQFLACISIDRYVAVTKVPSQSGVGKPCW-----IICFCVWMAAILLSIPQLVFYT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234
                                                                                                                                                                                                                                                                                    Gaps
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TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
                                                                                                                                                                                                                                                                                                                                                              10 DYYYEENEMNGTY---DYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIY 66
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OCT-1996 (Rel. 34, Last sequence update)
AMR-2002 (Rel. 41, Last annotation update)
chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (GPR-9-
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-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
BY SIMILARITY.
W; 6971F76F0A2484AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNDN---ARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Lautens L.L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M.,
                                                                                                                                                                                                                                  Length 369;
                                                                                                                                                                                                                     35.1%; Score v., 36.0%; Pred. No. 1.2e-32; +ive 77; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonner T.I.; submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                        ₹
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                                                                                                                                                                                                                                                                                    Matches 118; Conservative
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  280
304
322
369
369
198
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                                                                                                                                                                                                                                                          Similarity
  255
281
305
323
323
119
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01-0CT-1996
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P51686;
  TRANSMEM
DOMAIN
TRANSMEM
                                                                            DOMAIN
CARBOHYD
DISULFID
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                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                          Local
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CKR9_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.0%; Score 637; DB 1; Length 357; 36.5%; Pred. No. 1.6e-32; ive 74; Mismatches 115; Indels
                                                                                                                                                                                                                                                                      InterPro; IPR004069; Chemokine9_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
Fram; PP00101; 7m_1: 1.
PRINTS; PR0151; CHEMOKINE9.
PRINTS; PR01537; GPCRRHODOPSN.
PROSITE; PS0237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
G-PROFIED: Oupled receptor: Exansmembrane; Glycoprotein.
DOMAIN.

3.7 EXPRACELULIAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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(Rel. 39, Last sequence update)
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62 VVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAV-NAVHGWVLGKIMCKITSALYT 120 

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3 STESYFGTDD----YDNTEYYSIPPDHGPCSLEEVRNFTKVFVPIAYSLICVFGLLGNIM 58

121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCW----IICFCVWMAAILLSIPQLVF- 175

176 --YTVNDNARCIPIFPRYLGTS----MKALIQMLEICIGFVVPFLIMGVCYFITARTLMK 229  q

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230 MPNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTE

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                                                                                                                                                                                                              MEDLINE-99077268; PubMed-9862452;
Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
Albar J.P., Ardavin C., Marquez G.;
"Molecular cloning, functional characterization and mRNA expression
analysis of the murine chemokine receptor CCR6 and its specific ligand
                                                                                                                                                                                                                                                                                                      FEES Lett. 440:188-194(1998).

-1-FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MID-3-ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LENEY.

-1-SUBCELLULAR LOCATION: Integral membrane protein.

-1-SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
OCT-2001 (Rel. 40, Last annotation update) chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (KY411).
                                                               Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                     Yanagihara S., Komura E., Yanaguchi Y.;
"Mouse G protein-coupled receptor KY411.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1529; CHEWOKINBR6.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROFEIN_RECEP_F1_1; 1.
PROSITE; PS50263; G_PROFEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
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1 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR004067; Chemokine6_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
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BY SIMILARIT
                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB009369; BAA23776.1; -. EMBL; AJ222714; CAA10956.1; -.
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                                                musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001; 7tm_1;
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
367 AA;
                                                                                                                        SEQUENCE FROM N.A.
                                                                                         NCBI_TaxID=10090;
                              CCR6 OR CMKBR6.
                                                                                                                                                                                                                                                                                          MIP-3alpha.";
 16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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TRANSMEM
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Genomics 40:175-180(1897).

-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE, BINDS TO MIP-3-
ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
INTRACELLULAR CALCIUM IONS LEVEL.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                 8
                              26; Gaps
                                                                          8 STDYYYEENEMNGTYDYSQYELI-----CIKEDVREFAKVFLPVFLTIVFVIGLAGNSM 61
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Score 605, DB 1; Length 367; Pred. No. 1.4e-30; ); Mismatches 125; Indels ;

:09

Conservative

Similarity

Query Match Best Local Simi Matches 129; (

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33.3%; 37.9%;

MEDLINE=97313465; PubMed=9169459;
Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K., Nomiyama H., Yoshie O.;
"Identification of CCR6, the specific receptor for a novel lymphocyte-directed CC chemokine LARC.";
J. Biol. Chem. 272:14893-14898 (1997). P51684; Q92846; P78553; O1-OCT-1996 (Rel. 34, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) C-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (LARC receptor) (GPR-CY4) (GPRCY4) (Chemokine receptor-like 3) (CKR-L3) Euteleostomi; MEDLINE=97224503; PubWed=9070937; Liao F., Lee H.-H., Farber J.M.; "Cloning of STRL22, a new human gene encoding a G-protein-coupled receptor related to chemokine receptors and located on chromosome Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G., "Molecular cloning and RNA expression of two new human chemokine Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. SEQUENCE FROM N.A. Lautens L.L., Modi W., Bonner T.I.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases. McCoy R., Perlmutter D.H.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases Biochem. Biophys. Res. Commun. 227:846-853(1996) 374 AA CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3. MEDLINE=97040707; PubMed=8886020; SEQUENCE FROM N.A., AND FUNCTION STANDARD; receptor-like genes. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI\_TaxID=9606; SEQUENCE FROM CKR6\_HUMAN RESULT 8 CKR6\_HUMAN  127 133

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YYKKQRTKTDVYILNLAVADLLLETLPFWAV-NAVHGWVLGKIMCKITSALYTLNFVSG 126 73 FYKKARSMIDVYLLNMAIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINFNCG 132 MQFLACISIDRYVAVTKVPS----QSGVGKPCWIICFCVWMAAILLSIPQLVF---YTVN 179

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180 DNARCIPIFPRYLGTS----MKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKI

296 SCLNPILYVFMGASFKNYVMKVAKKYGSWRRQRQS 330

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
-i- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN NATURAL KILLER CELLS, MONCYTES, OR GRANULOCYTES.
-i- INDUCTION: BY INTERLEDVIN-2.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-i- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
TY (POTENTIAL).
TY (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
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D7F963534E990BC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; FRUGAZ, ANTO; 1.

PROSITE; PS00213; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein.

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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L -> V (IN REF. 4).
L -> V (IN REF. 5).
T -> S (IN REF. 5).
T -> S (IN REF. 4).
C -> L (IN REF. 4).
L -> L (IN REF. 4).
L -> F (IN REF. 4).
L -> F (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR000020; Anaphylatoxin. InterPro: IPR0004067; ChemoKine6_receptor. InterPro: IPR000276; GPCR_Rhodpsn. Pfam: PF000001; 7tm_1: 1.
                                                                                                                                                                                                 EMBL, U45984; AAB62714.1; --
EMBL, Z79784; CAB02144.1; --
EMBL, U60000; AAB0699.1; --
EMBL, U68030; AAC51124.1; --
HSSP, P34996; 1DDD.
GCRDb; GCR_1037; --
GCRDb; GCR_1037; --
GCRDb; GCR_1919; --
GCRDb; GCR_1941; --
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PRINTS; PR00237; GPCRRHODOPSN.
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182
192
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374 AA;
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15-JUL-1998 (Rel. 36, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (G protein-coupled
                                                                                                                                                                                                                                                    Cercopithecus aethiops (Green monkey) (Grivet).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AFULUS, 2. GPCR_Rhodpsn.

Interpro; IPR00276; GPCR_Rhodpsn.

Pfam; PF0001; 7tm_1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PRINTS; PS00237; GPCRHODOPSN.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

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EXTRACELLULAR (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
 309 CCLNPVLYAFIGOKFRNYFLKILKDLWCVRRKYKS 343
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-97373958; Pubmed-9230441;
                                                                                   15-JUL-1998 (Rel. 36, Created)
                                                             STANDARD
                                                                                                                                     receptor bonzo). CXCR6 OR BONZO.
                                                                                                                                                                                                          NCBI_TaxID=9534;
                                                             CCR6_CERAE
O18983;
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                                                  CCR6_CERAE
                                       RESULT
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Gaps

26;

Score 583; DB 1; Length 374; Pred. No. 3.2e-29; 68; Mismatches 120; Indels

32.1%; 36.1%;

Query Match 32.1% Best Local Similarity 36.1% Matches 121; Conservative

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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
01-MAR-2002 (Rel. 41, Last anno
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69
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343 AA;
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CCR6_MACNE
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                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                             72 QRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLA 131
                                                                                                                                                                          Gaps
                                                                                                                                                                                                        (G protein-coupled
                                                                                                                                                                                             12 YYEENEMMGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNARCI
                                                                                                                                                                                                                                                                                                                                                                                FRST. Hum. RELTOVITUSES 17:981-986(2001).
FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
                                                                                                                                                                                                                                                                                                                          186 PIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTV
                                                                                                                                                                                                                                                                                                                                              ----GYHDEEISTVVLATQMTLGFFLPLLAMIVCYSVIIKTLLHAGGFQKHRSLKIIFLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Margulies B.J., Hauer D.A., Clements J.E.; Identification and comparison of eleven rhesus macaque chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                       LINKED (GLCNAC. . .) (POTENTIAL).
6CBFE389C6E5919E CRC64;
                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                           291 VSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSK--TFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                             MGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                                                                                                                Score 581; DB 1; Length 342;
Pred. No. 3.9e-29;
1; Mismatches 130; Indels
       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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16-OCT-2001 (Rel. 40, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
02-X-C chemokine receptor type 6 (CXC-R6) (CXCR-6) (Greeptor bonzo) (G protein-coupled receptor STRL33).
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                                                                                              SIMILARITY
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                                                                                                                                                 31.9%;
                                                                                                                   39226
                                                                                                                                                             Similarity 34.2
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                                                                                                                     AA;
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Best Local Simi
Matches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LTCITVDRFIVVVKATKAYNQQAKRMTWGKVICLLIWVISLLVSLPQIIYGNVFNLDKLI 180
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01-MAR-2002 (Rel. 41, Last annotation update)
C-X-C chemokine receptor type 6 (CXC-R6) (G protein-coupled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LACISIDRYVAVTKVPS - - QSGVGKPCW - - IICFCVWMAAILLSIPQLVFYTV - - NDNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 CIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C----GYHDEEISTVVLATQMTLGFFLPLLAMIVCYSVIIKTLLHAGGFQKHRSLKIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHYEDDGFLNSFNDSSQEE----HQDFLQFRKVFLPCMYLVVFVCGLVGNSLVLVISIFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 TVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 VFMGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca nemestrina (Pig-tailed macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73; Mismatches 132; Indels
                                                                                                                                         EMBL, AF124380; AAD31419.1; -.
InterPro; IFR00275; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1: 1.
PRINTS: PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2: 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                           1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 1.6e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342
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237 MAVFLLTQTPFNLVKLIRSTHWEYYAMTSFHYT-----IIVTEAIAYLRACLNPVLYAF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 605163
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                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 LQSLTDVFLVNLPLADLVFVCTLPFWAXAGIHEWIFGQVMCKTLLGVYTINFYTSMLILT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNARCI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 PIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 VIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILYVF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 ORTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 YHEDYGLNSFNDSSQEE----HQDFLQFRKVFLPCMYLVVFVCGLVGNSLVLVISIFYHK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 YYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKK 71
                                                                                                                                                                                                                -I- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 CITVDRFIVVVKATKAYNQOAKRMTWGKVICLLIWVISLLVSLPQIIYGNVFNLDKLIC-
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                                                                                    SEQUENCE FROM N.A. MEDINE-9737958; PubMed-9230441; MEDINE-9737958; PubMed-9230441; Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.; Expression cloning of new receptors used by simian and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 342;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
39297 MW;
                                                                                                                                                                         immunodeficiency viruses.";
Nature 388:296-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 31.39
Best Local Similarity 33.69
Matches 119; Conservative
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187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294
102
16
342 AA;
                                           NCBI_TaxID=9545;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCRE_HUMAN STANDARD; PRT; 342 AA.
COGRE_HUMAN STANDARD;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 41, Last annotation update)
CA-C chemokine receptor type 6 (CXC-R6) (CXCR-6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "STRL33, A novel chemokine receptor-like protein, functions as a distance offactor for both macrophage-tropic and T cell line-tropic HIV-1.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
---SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                         VSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSK--TFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDINE-973041; MEDINE-9737958; PubMed-9230441; Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.; Expression cloning of new receptors used by simian and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A., Farber J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1. PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-97311099; Pubmed-9166430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Exp. Med. 185:2015-2023(1997).
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EMBL; U73529; AAB61456.1; --
EMBL; U73531; AAB61457.1; --
EMBL; Y13248; CAA73698.1; --
GCRDb; GCR_1328; --
GCRDb; GCR_1330; --
306 MGASFKNYVMKVAKKYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunodeficiency viruses.";
Nature 388:296-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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ъ,
G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycoprotein; Polymorphism.
32
EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                         132 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNARCI 185
                                                                                                                                                                                                                                                                                                                                                                            72 ORTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLA 131
                                                                                                                                                                                                                                                                                                                                                                                          62 LOSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYTINFYTSMLILT 121
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                6 YHEDYGFSSFNDSSQEE----HQDFLQFSKVFLPCMYLVVFVGGLVGNSLVLVISIFYHK 61
                                                                                                                                                                                                                                                                                                                                 12 YYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKR4_HUMAN STANDARD; PRT; 360 AA.
P51679; Q9ULX6; Q9ULX7;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 4 (C-C CKR-4) (CC-CKR-1) (CCR-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                       186 PIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 VIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 MAVFLLTQMPFNLMKFIRSTHWEYYAMTSFHYT----IMVTEAIAYLRACLNPVLYAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                     D (GLCNAC. . .) (POTENTIAL). (IN STRL33.3).
                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 MGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 VSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSK--TFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Spleen;
MEDLINE-95370289; PubMed-7642634;
Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
                                                                                                                                                                                                                                                                                         Length 342;
                                                                                                                                                                                                                                                                                                             75; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                             1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                         3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUAR (POTENTIAL).
                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                    9FBC025556D1082E CRC64;
                                                                                                                                        5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                        Score 560; DB 1;
Pred. No. 7.4e-28;
                                                                                                                                                                                                                                          003506
                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                              6 (POTENTIAL)
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N-LINKED (GLC
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                                                                                                                                                                                                                                                                                                  Similarity
                     coupled
                                                        NCBI_TaxID=9606;
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                        G-protein
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TRANSMEM
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                                                                                                           SECUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
MEDLINE-21040311; PubMed=11196669;
Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
Hirai K., Tokunaga K.
"New variations of human CC-chemokine receptors CCR3 and CCR4.";
Genes Immun. 1:97-104(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemokine, and 1:309.";

J. Immunol. 164:4048-4054(2000)

-1- FUNCTION: HIGH AFFINITY RECEPTOR FOR THE C-C TYPE CHEMOKINES

TRAC/SCYA17 AND MOC/SCYA22. THE ACTIVITY OF THIS RECEPTOR IS

MEDIATED BY G(1) PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM. CAN FUNCTION AS A CHEMOATTRACTANT
HOMING RECEPTOR ON CIRCULATING MEMORY LYMPHOCYTES AND AS A
CORECEPTOR FOR SOME PRIMARY HIV-2 ISOLATES. IN THE CNS, COULD
MEDIATE HIPPOCAMAL.NEURON SURVIVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE THYMUS, IN TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE THYMUS, IN PERSON DERIVORTED STATES. INCLUDING T CELLS, WOSTLY CAP4 CELLS, AND BASOPHILS, AND IN DATESTED ALSO IN MACROPHAGES, IL-2-ACTIVATED NATURAL KILLER CELLS AND SKIN-HOMING MEMORY T CELLS, MOSTLY THE ONES EXPRESSING THE CUTAMBOUS LYMPHOCYTE ANTIGEN (CLA). EXPRESSED IN BRAIN MICROVASCULAR AND CORONARY ARTERY ENDOTHELIAL CELLS. PROSPHOSYL IN IN NATURAL KILLER CELLS, SCYAZZ BINDING INDUCES PROSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY BY SHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY BY BETA-ADRENCED RECEPTOR KINASES I AND 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
Yoshie O., Gray P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P., Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher B.C., "The chemokine receptor CCR4 in vascular recognition by cutaneous but not intestinal memory T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဌ
                               novel CC chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20219238; PubMed-10754297; Inngjerdingen M., Damaj B., Maghazachi A.A.; "Human NK cells express CC chemokine receptors 4 and 8 and respond thymus and activation-regulated chemokine, macrophage-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                          Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.; The T cell-directed CC chemokine TARC is a highly specific biological ligand for CC chemokine receptor 4."; J. Biol. Chem. 272:15036-15042(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Macrophage-derived chemokine is a functional ligand for the CC chemokine receptor 4.";
                     "Molecular cloning and functional expression of a receptor cDNA from a human basophilic cell line."; J. Biol. Chem. 270:19495-19500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 273:1764-1768(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98104168; PubMed=9430724;
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Proudfoot A.E.I., Wells T.N.C.;
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EMBL; AB023888; BAA86965.1; -.
EMBL; AB023889; BAA86966.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor 4.
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1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS. CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACITVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
                                                                                                                                                                                                                                                                             Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
DATABASE: NAME-PROM; NOTE-CD guide CD4128b entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd4128b.htm".
     High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (GRO/MGSA
                                                                                                                                                                                                                                                                                                           "Molecular characterization of receptors for human interleukin-9, {\tt GRO/melanoma} growth-stimulatory activity and neutrophil activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Placenta;
MEDLINE-95014476; PubMed-7929358;
Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
"Comparison of the genomic organization and promoter function for human interleukin-8 receptors A and B.";
J. Biol. Chem. 269:26381-26389(1994).
                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.; "Structure, genomic organization, and expression of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92355587; PubMed-1379593;
Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wor
"Characterization of two high affinity human interleukin-8
                                                                                                                                                             Murphy P.M., Tiffany H.L.; "Cloning of complementary DNA encoding a functional human interleukin-8 receptor."; Science 253:1280-1283(199).
                receptor) (IL-8 receptor type 2) (CDw128b). IL8RB OR CXCR2.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-93205012; PubMed-8384312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           interleukin-8 receptor B gene.";
J. Biol. Chem. 269:11065-11072(1994).
                                                                                                                               SEQUENCE FROM N.A. MEDLINE-91368200; PubMed-1891716;
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94209273; PubMed-7512557;
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EMBL; M94812; AAA1460.1; --
EMBL; L19593; AAA1460.1; --
EMBL; L19593; AAB59437.1; --
EMBL; U11869; AAB60656.1; --
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interleukin-8 receptor
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PIR; A53611; A53611.
HSSP; P34996; 1DDD.
GCRDb; GCR_0077; -.
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CYTODIASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                         InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00202; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Phosphorylation; Polymorphism.
                                                                                                                                                                                                                                                                                                          4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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(Rel. 40, Last anno
EMBL; AB023890; BAA86967.1; -. EMBL; AB023891; BAA86968.1; -. EMBL; AB023892; BAA86969.1; -.
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Best Local Similarity 35.8°
Matches 115; Conservative
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01-FEB-1996
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                                                                              PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.
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33.2%; Pred. No. 2.8e
tive 75; Mismatches
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                                               InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000832; GPCR_secretin.
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GCR_1339; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial
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affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).
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                                          Euteleostomi;
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MEDLINE-96175151; PubMed-9110929;
Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
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                       Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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InterPro; IPR000832; GPCR_secretin
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353 AA;
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                                                                NCBI_TaxID=9598;
             LEBRB OR CXCR2.
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Human CCR7 protein
Human CCR7 Protein

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7TM receptor prote Human CCR9a prote1 Epstein Barr virus G-protein coupled

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BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis; cell proliferation; anti-inflammatory; anti-anglogenic; antitumor; HIV; anti-allergic; antiviral.
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                                                                                       AAY57292
AAM99949
AAY30126
ABB11162
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ABB10276
AAU18115
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AAU18669
AAU21655
AAR53745
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WPI; 1999-620375/53.
N-PSDB; AAZ90528.
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WO9952945-A2.
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16-APR-1999;
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                                                                                                                             August 6, 2002, 17:57:40; Search time 32.78 Seconds
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1 MALEQNQSTDYYYEENEMNG.....VEEFPFDSEGPTEPTSTFSI
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                      747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAW93169
AAY94325
AAG80119
AAU08994
AAG67237
AAB62389
AAW93170
AAY30125
AAY71301

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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represents the full-length human BGCKr protein
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                                                                                                           Conservative
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                                                                                                      Local Similarity
                                                                                  350 AA;
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                                                                                                            Matches 350;
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                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                               cancer;
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    Claim
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treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2; treatment; FIAO41 protein; gene therapy; immune response; vaccrie; HIV-1; cancer; diabetes; anorexia; bullimia; Parkinson's disease; acute heart failure; hypotension; hypertension; uniary retention; osteoporosis; allergy; angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia; benign prostatic hypertrophy; psychotic disorder; neurological disorder; anxiety; manic depression; delirium; dementia; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; linkage analysis; gene mapping; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HFIA041; G-coupled receptor; disease susceptibility; diagnosis; immunise;
                                                                                                                                                                       The present sequence represents a human signal peptide-containing protein (SP), designated SP-16. SP proteins can be used to stimulate cell proliferation or to treat or prevent cancer. SP antagonists are also used to treat or prevent cancer, and also for treating or preventing neuronal disorders or immune responses. Polynucleotide sequences complementary to the SP-encoding polynucleotides are useful for the detection of SP-encoding nucleic acid molecules in biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180
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Reddy
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Lal P,
                                     WPI; 1999-337694/28
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tes 350; Conserv
                                                                                                                                                                                                                                                                                                                                                               350 AA;
                                                          N-PSDB; AAX61288
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  Au-Young J,
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                                                        The invention relates to a human BGCKr protein, a G-protein coupled receptor. The BGCKr protein can be expressed by standard recombinant methodology. BGCKr are receptor proteins possibly involved in modulation of profulflammatory or stimulatory functions of chemokines; cell proliferation, migration, adhesion and targeting, and excoytosis. The BGCKr nucleic acids and derived proteins (or their variants), antibodies and modulators are potentially useful for modulating inflammation: chemoattractant activity of leucocytes; angiogenesis; cell proliferation; tumour growth, allergic reactions and entry of human immune deficiency virus into cells, for therapeutic or prophylactic purposes. They are also used for diagnosis and in drug-screening assays. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal peptide-containing protein; SP; cell proliferation; neuronal disorder; immune response; detection.
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                                                                                                                                                                                                                                                                                                                                                                                   Length 350;
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100.0%; Pred. No. 1.6e-195;
tive 0; Mismatches 0; I
                         Fig 2A-B; 123pp; English.
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                                                                                                                                                                                                                                                                                      New G-coupled receptor (HFIAO41) polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of cancer, HIV infections and Parkinson's disease
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                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 22-23; 27pp; English.
                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                      97US-0962922.
97US-0055895.
                                                                     98EP-0301170.
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Best Local Similarity 100.
Matches 350; Conservative
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                                                                                                                                                                                                                                                    N-PSDB; AAX22557
                                                                     17-FEB-1998;
                                                                                                         27-OCT-1997;
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EP899332-A2.
                                  03-MAR-1999
                                                                                                                                                                                               Ellis CE;
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The present sequence is VSHK-1, a new seven transmembrane receptor which contains seven membrane-spanning helical domains that are linked by three intracellular and three extracellular loops. The gene sequence encoding VSHK-1 was isolated from a cDNA library. In heart tissue, where VSHK-1 is predominantly found, three RNA species were identified: a 1.3kb; a 2.0kb; and a 5.0kb species. The polynucleotide encoding the present sequence corresponds to the 2.0kb form. The 1.3kb form may result from the use of an alternative polyadenylation site while transcription of a 3.0kb intron at nucleotide 74 could account for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.0kb species. VSHK-1 polynucleotides can be used as hybridisation probes
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                                                                                                                                                                                                                                                                                                                                                                                                Human; seven transmembrane receptor; VSHK-1; signal transduction.
"potential N-glycosylation site"
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/label= Transmembrane_domain
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06-JAN-1999;
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to detect and measure VSHK-1 mRNA. They may also be used to identify substances that modulate the level of VSHK-1 mRNA. The VSHK-1 coding sequence can be integrated into an expression vector for production of VSHK-1 receptor polypeptides in host cells. The polypeptides can be used to identify agents which modulate VSHK-1 receptor signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                    MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                     Diagnostic agent containing two or more receptor-specific ligands,
                                                                                                                                                                                                                                                                                                      NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
                                                                                                                                                        MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS
                                                                                                                                    .;
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                                                                                                               Length 350;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                              Score 1819; DB 21;
Pred. No. 1.6e-195;
                                                                                                                                    ő
                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG80119 standard; Protein; 350
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0
                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antirheumatic; antiarthritic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IPFP-) IPF PHARM GMBH. (FORS/) FORSSMANN U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human CCR11 protein.
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                                                                                                                           Similarity
                                                                               350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200172830-A2.
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                                                                                                                Query Match
Best Local Simi
Matches 350;
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                                                                                  Sequence
                                                          activity
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This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (Theumatoid arthritis or lupus), where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone carron diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antiasthmatic, immunosuppressive, dermatological, antirheumatic, antiarthritic.

Commonsupersistic of the invention and inflammatory calls through a constellation of these cells. AdG80045-AAG80128 represent human chemokine cyclification of these cells. AAG80045-AAG80128 represent human chemokine
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for detecting tumors, inflammation etc., also therapeutic use of inhibitors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiatherosclerotic; analgesic; cytostatic; antianginal; cardiovascular disorder; anglogenesis-related disorder; neural disorder; pain response disorder; inflammatory disorder; atherosclerosis; angina pectoris; myocardial infarction; ischaemic heart disease; sudden cardiac death; obesity; hypertensive heart disease; diabetes; prostate cancer-related pain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1819; DB 22; 100.0%; Pred. No. 1.6e-195;
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                                                       German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 350
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                                                       Page 11; 26pp;
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Best Local Similarity 100.
Matches 350; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            350 AA;
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                                                         Disclosure;
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Homo sapiens

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05-MAR-2001; 2001WO-US07073.
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(first entry)
                                                                                                                                                                                                                                                                                                                                               Schweickart VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        phenomenon and migraine
                          acid sequence
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                                                                                                                                                                       Homo sapiens.
13-NOV-2001
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Matches 350;
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                                                                                                                                                                                                                                                                                                                                                Gray PW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                           The invention relates to novel human G protein-coupled receptors (GPCR) named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and nucleic acids encoding them are useful for identifying agents for the treatment of cardiovascular disorders, angiogenesis-related disorders, neural disorders, pain response disorders and inflammatory disorders e.g. atherosclerosis, angina pectoris and myocardial infarction, isonaemic heart disease, sudden cardiac death, hypertensive heart disease, databetes, prostate cancer-related pain, diabetes and obesity. The present sequence represents GPCR 2398.
                                                                                                                                                                                                                                                                Novel G protein coupled receptors and nucleic acids encoding them, for identifying agents for the treatment of cardiac disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180
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125..141
/label- G_protein_receptor_signature
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                                                                                                                                                                                                                                                                                                      Claim 9; Fig 9; 209pp; English.
                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
                                                                                                                 28-FEB-2001; 2001WO-US06543
                                                                                                                                           29-FEB-2000; 2000US-186059P
                                                                                                                                                                                                                         WPI; 2001-589866/66.
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Best Local Similarity
Matches 350; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 AA;
                                                                                                                                                                                                                                     N-PSDB; AAS14572.
                                                                                                                                                                                                Glucksmann MA,
                                                            WO200164882-A2
                                                                                       07-SEP-2001
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            Key
Region
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                                                                  Human; chemokine receptor; CCRII; G protein coupled receptor; inflammatory disease; heumatory disease; heumatoris inflammatory bowel disease; asthma; angiogenesis; artherosclerosis vascular association disease; hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenn; left ventricular diastolic dysfunction; migraine; preterm labour; oesophageal spasm; ischemic stroke; subarachnoid haemorrhage; myocardial infarction; congestive heart failure; endometriosis; vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An isolated polynucleotide encoding the chemokine receptor CCRII, useful for treating rheumatoid arthritis, inflammatory bowel disease, asthma, angiogenesis, artherosclerosis, cardiac arrhythmias, Raynaud's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the human chemokine receptor CCRII.

CCRII is a member of the G protein coupled receptor family. A CCRII
polypeptide, its inhibitor, an antibody, or other modulator of CCRII
expression or biological activity, is useful for treating many
inflammatory diseases, for example, rheumatoid arthritis, inflammatory
bowel disease, and asthma. They are also useful for treating
anglogenesis, artherosclerosis vascular association diseases which may
include but are not limited to hypertension, angina pectoris, cardiac
arrhythmias, left ventricular disstolic dysfunction, Raynaud's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
stroke, subarachnoid haemorrhage, myocardial infarction, congestive
heart failure, endometriosis, vasospasm, retinopathy, nephropathy, or
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of human chemokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epp A, Raport CJ,
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HFIAO41; G-coupled receptor; disease susceptibility; diagnosis; immunise; treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2; incoulate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer; diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure; hypotension; hypertension; urlary retention; osteoporosis; allergy; angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia; ansiety; manic depression; delirium; dementia; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; linkage analysis; gene mapping; human; ss.
                                                                                                                                                                                                                                                                                                                            61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
                                                                                                                                                                                                                                                                                                                                                                                                              LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNP 300
                                                                                                                                                                                                        New G-coupled receptor (HFIAO41) polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of cancer, HIV infections and Parkinson's disease
                                                                                                                                                                          1 MALEQNOSTDYYYEENEMNCTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
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                                                   Score 1819; DB 22;
Pred. No. 1.8e-195;
Mismatches 0;
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100.0%;
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970S-0055895.
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                                                                                                                      Conservative
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                                                                                     Similarity
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated or recombinant chemokine receptor (designated CCX CKR) polypeptide (Pl) or its fragment, useful for identifying CCX CKR modulators which can be used in the treatment of inflammation, allergy,
narcipifprylgtsmkaliqmleicigfvvpflimgvcyfitartlmkmpnikisrplk 240
                                                                                                                300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemokine receptor; CCX CKR; chemokine; ELC; SLC; TECK; modulator; antinflammatory; immunosuppressive; cytostatic; antiallergic; human; immunostimulant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schall TJ;
                                                                                  VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNP
                                                                                                                                                                                                        350
                                                                                                                                                                          301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanley M, Miao Z,
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371
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99US-0159210.
99US-0172979.
99US-0173389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-1999;
20-DEC-1999;
28-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB62389;
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Ohno T;

Koshio

98WO-JP05886 97JP-0354537

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New seven-pass transmembrane receptor protein useful for treating, preventing or diagnosing autoimmune diseases
                                                                                                                                                                                                                                                                                                                   Claim 1; Page 101-103; 118pp; Japanese.
                                                                                                                                                       (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                    WPI; 1999-493806/41.
                                                                                                                                                                                                                                       N-PSDB; AAX86674
 Homo sapiens.
                                                                                                                          24-DEC-1997;
                                                                                            24-DEC-1998;
                                                             08-JUL-1999
                                                                                                                                                                                        Ishimaru H,
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                                     This sequence encodes a G-coupled receptor, HFIA041 which is useful for diagnosing susceptibility to diseases by detecting mutations in the HFIA041 gene, and can diagnose diseases associated with HFIA041 protein imbalance by determining HFIA041 polypeptide expression levels. Agonists and antagonists of the protein can be used in treatment to activate diagnosity or inhibit (arregonist) HFIA041 activity, in addition to direct administration of antisense sequences to prevent expression, or HFIA041 conditions associated with a lack of FIA041 polypeptide expression. HFIA041 antibodies are useful for inducing an immune response to immunise and prevent disease, and for isolating immune response to immunise and prevent disease, and for isolating collipseptides or purifying the Polypeptides by affinity chromatography. HFIA041 polypeptides can be administered directly or as a vaccine to inculate against disease. Diseases diagnosed, prevented and treated conclude bacterial, fundal, protozoan and viral infections, particularly HY-1 or -2 infections; cancer; diabetes; anorexis; bulimia; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary cetention; esteoporosis; angina pectoris; myocardial infarction; ulcers; asthma: allergies; benign prostatic hypertrophy; and psychotic and neurological disorders, including anxiety, schizophrenia, manic cetention, osteoporosis; angina pectoris; myocardial infarction and dyskinesias such as Huntlington's disease or Gilles de la Tourette's syndrome. The HFIA041 polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.7%; Score 1814; DB 20; Length 349; 100.0%; Pred. No. 5.8e-195; 1.4e 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 LYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seven-pass transmembrane receptor; autoimmune disease; white blood cell dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human seven-pass transmembrane receptor protein.
              Page 25-26; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY30125 standard; Protein; 350 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 349; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-0CT-1999
              Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 vlltvvivfivtglpynivkfcraidiiyslitscdmskrmdiaiqvtesialfhsclnp 300
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                                                                                                                                                                                                                                                                                         MVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
                                                                                                                                                                                 Gaps
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The present sequence represents a seven-pass transmembrane receptor protein. The protein and its DNA can be used to screen substances for the diagnosis, prevention and treatment of autoimmune diseases, particularly those due to white blood cell dysfunction.
                                                                                                                                                                                                                                      1 MALEQNQSTDYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                   NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNP
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                                                                                                                                              Length 350;
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                                                                                                                                                                                 Indels
                                                                                                                                              Score 1814; DB 20;
Pred. No. 5.8e-195;
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                                                                                                                                            Query Match
Best Local Similarity 99.7
Matches 349; Conservative
                                                                                        350 AA;
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                                                                                           Seguence
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(first entry)
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N-PSDB; AAA46029.
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                                                                                                                                                                                                                                                                                                                                         WO200022131-A2.
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03-SEP-1999;
29-SEP-1999;
                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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28-MAY-19
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12-MAR-1
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                                                                                                                                                                                                                                                                                                                                                                                  Novel human orphan G protein-coupled receptors and the encoding cDNAs for use in the identification of G protein-coupled receptor agonists
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                                                                                                                                                                                                                                                                                                                                                                                                               Claim 42; Page 69-70; 102pp; English.
                                                                                                                                                                                                                                                                                                                                   Lin I;
                                                                                      99US-0121852.
99US-0123946.
99US-0123949.
                                                                                                                                                                                                                                                                                                                                 Dang HT, Liaw CW,
                                                                                                                    99US-0136436
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99US-0157282
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N-PSDB; AAD01128.
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es 348; Conserv
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        WO200031258-A2
                                                                                                                                                                                                                                                                                                               (AREN-) ARENA
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28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
29-JUN-1999;
29-SEP-1999;
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29-SEP-1999;
29-SEP-1999;
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01-OCT-1999;
01-OCT-1999;
01-OCT-1999;
01-OCT-1999;
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16-FEB-1999;
26-FEB-1999;
                                                13-OCT-1999;
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28-MAY-1999;
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                           02-JUN-2000
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Matches
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NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
                                                                                                                                                                                                                                                                                                                                                                                         Human; G protein coupled receptor; GPCR; transmembrane receptor; identification; agonist; screening; therapeutic; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dang HT;
                                                                                                                                                                                                                                                                                                                                                          Human G protein coupled receptor hPPR1 protein SEQ ID NO:24
                                                                                                                                                                                      301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
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Lin I, Lowitz K, White C;
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990S-0136436.
990S-0136437.
990S-0137127.
990S-0137131.
990S-0141448.
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9805-0109213.
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9905-0120416.
9905-0121852.
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05-JUN-2000 (first entry)
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                                                     The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46617 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; TSC; tuberous sclerosis complex; cytostatic; antimicrobial; osteopathic; antiulcer; antiasthmatic; antiallergic; neuroprotective; cardiant; hypotensive; hypertensive; nootropic; anticonvulsant; analgesic; tranquiliser; immunosuppressive; antinflammatory; gene therapy; TSC7; infection; cancer; autoimmune disorder; Parkinson's disease; osteoporosis; neurological disorder.
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                                                                                                                                                                                                                                                                                                          LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180
                                                                                                                                                                                                                                                                                                                                                      VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
Non-endogenous, human G protein-coupled receptors for screening
                                                                                                                                                                                                                            ;
                                                                                                                                                                                                       Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1810; DB 21;
Pred. No. 1.6e-194;
                                                                                                                                                                                                                            0; Mismatches
                                 Example 1; Page 99-100; 187pp; English.
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                                                                                                                                                                                                      99.5%;
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Matches 348; Conservative
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The present sequence is human tuberous sclerosis complex 7 (TSC7).

TSC7 polynucleotides and polypeptides are useful for determining the presence or predisposition to a disease associated with altered levels of TSC7. TSC7 polynucleotides, polypeptides and antibodies specific for the polypeptide are useful for treating or preventing pathological conditions associated with the disorder in a G-protein mediated pathway. They are useful for diagnosing a hyperproliferative condition such as a neoplasm or dermatological condition. TSC7 nucleic acids and polypeptides are useful in the treatment of microbial infections, pain, cancer, anorexia, asthma, autoimmune disorders, parkinson's disease, acute heart failure, hypo/hypertension, osteoporosis, multiple sclerosis, angina pectoris, myocardial infarction, ulcers, allergies, benign prostatic hypertrophy and psychotic and neurological disorders, including schizophrenia, dementia, severe mental retardation and dyskinesias, such as the funtington's disease and/or other pathologies and disorders. TSC7 polypeptides are also useful as immunogens to produce antibodies and as
                                                                                                                                                                                                                                                                          Novel nucleic acid encoding G-protein coupled receptor for diagnosis and treatment of conditions associated with disorder in a G-protein mediated pathway such as cancer, neurological disorders and infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1808; DB 21;
Pred. No. 2.7e-194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 8; 132pp; English.
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20-APR-2000; 2000US-0556002
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Matches 348; Conservative
                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                2000-679670/66
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Best Local Similarity
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                                                                                                                      Gould-Rothberg BE;
                                                                                                                                                                                                             N-PSDB; AAC68722
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The invention relates to a human BGCKr protein, a G-protein coupled receptor. The BGCKr protein can be expressed by standard recombinant mathodology. BGCKr are receptor proteins possibly involved in modulation of proinflammatory or stimulatory functions of chemokines; cell proliferation, migration, adhesion and targeting, and exocytosis. The BGCKr nucleic acids and derived proteins (or their variants), antibodies and modulators are potentially useful for modulating inflammation; chemoattractant activity of leucocytes; angiogenesis; cell proliferation; tumour growth; allergic reactions and entry of human immune deficiency virus into cells, for therapeutic or prophylactic purposes. They are also used for diagnosis and in drug-screening assays. The present sequence represents the sequence of a partial human BGCKr protein.
                                                                        BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis; cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV; anti-allergic; antiviral.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 MNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKKQRTKTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding human BGCKr receptor, used e.g.
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Pred. No. 2.5e-185;
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100.0%; Pred. No. 2.5e-
--:va 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulating inflammation and tumor growth
                         Human BGCKr partial amino acid sequence
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Matches 333; Conservative
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                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                      WO9952945-A2
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16-APR-1999;
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                                                                                                                                                                                                                                                                                                               Human; chemokine receptor; CCRII; G protein coupled receptor; inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; asthma; angiogenesis; artherosclerosis vascular association disease; hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon; left ventricular diastolic dysfunction; migraine; preterm labour; myocardial infarction; congestive heart failure; endometriosis; vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the bovine chemokine receptor CCRII. CCRII is a member of the G protein coupled receptor family. A CCRII polypeptide, its inhibitor, an antibody, or other modulator of CCRII expression or biological activity, is useful for treating many inflammatory diseases, for example, rheumatoid arthritis, inflammatory bowel disease, and asthma. They are also useful for treating and angiogenesis, artherosclerosis vascular association diseases which may include but are not limited to hypertension, angina pectoris, cardiac arrhythmias, left ventricular diastolic dysfunction, Raynaud's phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic stroke, subarachnoid haemorrhage, myocardial infarction, congestive heart failure, endometriosis, vasospasm, retinopathy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated polynucleotide encoding the chemokine receptor CCR11, useful for treating rheumatoid arthritis, inflammatory bowel disease, asthma, angiogenesis, artherosclerosis, cardiac arrhythmias, Raynaud's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 MYVAIYAYYKKQRTKTDVXILNLAVADLLLLFTLPPWAVNAVHGWVLGKIMCKITSALYT 120
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                                                                                                                                                                                                                                                     Amino acid sequence of bovine chemokine receptor CCR11.
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86.0%; Pred. No. 3.5e-173;
iive 27; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epp A, Raport CJ,
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                                                          AAG67238 standard; Protein; 350 AA.
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2000US-0187231.
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                                                                                                                                                                                             (first entry)
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03-MAR-2000;
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Best Local S
                                                                                                                            AAG67238;
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15
                           AAG67238
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Search completed: August 6, 2002, 18:08:09 Job time: 629 sec

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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIR=BALB/C;
MEDLINE=20519697; PubMed=11063828;
Dorf M.E., Berman M.A., Tanabe S., Heesen M., Luo Y.;
"Astrocytes express functional chemokine receptors.";
Neurocimmunol: 111:109-121(2000).
EMBL; AF306532; AAK81712.1;
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Last annotation update)
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ilarity 85.4%; Pred. No. 1.6e-133;
Conservative 26; Mismatches 25;
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Best Local Similarity
Matches 299; Conserv
 Receptor.
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Q91zh4 rattus norv
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Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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01-OCT-2001 (TrEMBLrel. 18, Last annotation update) CHEMOKINE RECEPTOR CCR9 (CC CHEMOKINE RECEPTOR 9A).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                      NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-HARLAN SPRAGUE-DAWLEY;

Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;

Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;

Identification and characterization of novel G-protein coupreceptors expressed in regenerating peripheral nerve.";

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF090348; AAG24470.1; -.

R Pfam; PF00001; 74m_11 1.

R PROSITE; PS00237; GPCRRHODOPSN.

R PROSITE; PS00237; GPCRRHODOPSN.

R PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 221;
                                                                                                                                 301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE G-PROTEIN COUPLED RECEPTOR GPCR14 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24342 MW; 5622DD6073738A6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.1%; Score 912; DB 11;
83.3%; Pred. No. 3.9e-73;
Live 19; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 169; Conservative
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 2
221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                           09ESK1;
01-MAR-2001 (
01-MAR-2001 (
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NON_TER
SEQUENCE
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090006;
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                                   181
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Q9ESK1
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Yu C.-R., Peden K.W.C., Farber J.M.;
"CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : : |||:|||:|: SCVLLIMCISVDRYIAIAQ-----AMRAHTWREKRLLYSKWVCFTIWVLAAALCIPEILY 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGMQFLACISIDRYVAVTKVPSQSGVGKPCW-----IICFCVWMAAILLSIPQLVF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 YTVNDN----ARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 SSKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 IYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFV 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
MEDINE-99248139; Pubmed-10229797;
MEDINE-99248139; Pubmed-10229797;
Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
Ziaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
Ziaballication of the orphan chemokine receptor GPR-9-6 as CCR9,
receptor for the chemokine TECR.";
J. Immunol. 162:5671-5675(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSBLVO;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 19, Last annotation update)
CC CHEMOKINE LARC SPECIFIC RECEPTOR.
MCCR6.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 NOSTDYYYEE-NEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQIKEESGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKK
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.3%; Score 643; DB 4; Length 369; Best Local Similarity 36.4%; Pred. No. 4.5e-49; Matches 120; Conservative 75; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 AA; 42015 MW; F27CEA0CFB66B44C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1531; CHEMOKINER9.
PRINTS; PRO0237; GPERRHODODSN.
PROSITIE; PSO0237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITIE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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EMBL, AF145439; AAF66699.1; -...
InterPro: IPR004069; Chemokine9_receptor.
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCW----IICFCVWMAAILLSIPQLVF- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --YTVNDNARCIPIFPRYLGTS----MKALIQMLEICIGFVVPFLIMGVCYFITARTLMK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 MPNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STDYYYEENEMNGTYDYSQYELI -----CIKEDVREFAKVFLPVFLTIVFVIGLAGNSM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TERBLE-1. 05, Last sequence update)
01-DEC-2001 (TERBLE-1. 19, Last annotation update)
CHEMOKINE RECEPTOR.
CHEMOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 KKYELQDRDVC---EPRYRSVSEPITWKLLGLGLELFFGFFTPLLFMVFCYLFIIKTLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of two chemokine receptor homologs (CXC-R4 and CC-R7) in rainbow trout Oncorhynchus mykiss.";
J. Leukoc. Biol. 65:684-690(1999).
EMBL; AJ003159; CAA05917.1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99260342; PubMed-10331499;
Daniels G.D., Zou J., Charlemagne J., Partula S., Cunningham C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                        Molecular Cloning of Murine Homologue of CCR6, the Specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                           Submitted (Jul-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AB016031; BAA82443.1; -. HSSP; P34996; 1DDD. HSSP; P34996; 1DDD. InterPro; IPR000407; Chemokine6_receptor. InterPro; IPR0004076; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1. PRINTS; PR01529; CHEMOKINER6. PRINTS; PR00237; GPCRRHODOPSN. PROSITE; PS00237; GPCRRHODOPSN. PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 SIALFHSCLNPILYVFMGASFKNYVMKVAKKYGSWRRQRQ 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| ||||||||| |:: | |:| |:| |:| |:: | |:: | |:: | |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 611; DB 11;
Pred. No. 3e-46;
0; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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38.2%;
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042444;
01-JAN-1998 (TrEMBLEEL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                           for CC Chemokine LARC.
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                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secompes C
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Poehlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W., Kirchhoff \rm F.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 LACISIDRYVAVTKVPSQSGVGKP----CWIICFCVWMAAILLSIPQLVFYTVND---NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVL
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"Simian immunodeficiency virus utilizes human and sooty mangabey not rhesus macaque STRL33 for efficient entry.";
J. Virol. 74:5075-5082(2000).
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                                                                                                                                                                                                                                 Length 368;
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InterPro; IPR000276; GFCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHDOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SEQUENCE 343 AA; 39589 MW; A75B7A0751C13455 CRC64;
                                                                                                                                             41523 MW; BE28E2D4C47E821A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                           Query Match 32.2%; Score 586.5; DB 13; Best Local Similarity 37.3%; Pred. No. 4.5e-44; Matches 120; Conservative 58; Mismatches 125;
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Q9BDS6;
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"A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzo.";
Nat. Immunol. 1:298-304(2000).
EMBL; AF301018; AAG34367.1: -.
                                                                                                                                                     70 KKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQF 129
                                                                                                                                                                                                                                        LACISIDRYVAVTKVPS--QSGVGKPCW--1ICFCVWMAAILLSIPQLVFYTV--NDNAR 183
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                                       Gaps
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                                                                                                 184 CIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 VFMGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
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                                       Indels
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Last annotation update)
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InterPro; IPR000276; GPCR_Rhodpsn.
PRIMTS; PR001; 7tm.1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                Mismatches 131;
                 Pred. No. 2.4e-43;
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MEDLINE-21177382; PubMed-11017100;
33.78; Pic.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
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             Similarity
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Best Local Similarity
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             Local
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          Best Loc
Matches
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MEDLINE-21134756; PubMed-11242524;
MEDLINE-21134756; PubMed-11242524;
Made-Evans A.M., Russell J., Jahkins A., Javan C.;
Cloning and sequencing of cynomolylus macaque ccr3, gpr15, and str133:
Cloning and sequencing of cynomolylus macaque ccr3, gpr15, and str133:
Dotential coreceptors for HIV type 1, HIV type 2, and SIV.";
AIDS RES. Hum. Retroviruses 17:371-375(2001).
EMBL, AF291671; ARX25742.1;
EMBL, AF291671; ARX25742.1;
PFAMTY, PRO00276; GPCR-Rhodpsn.
PROSTE; PE000277; GPCREHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; UNKNOWN_1.
                                              NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
SMLTLTCITVDRFIVVVQATKAFNRQAKWK-IWGQVICLLIWVVSLLVSLPQIIYGHVQD 183
                                                                                        184 IDKLI---CQYHSEEISTMVLVIQMTLGFFLPLLTMILCYSGIIKTLHARNFQKHKSLK 240
                                                                                                                                                       VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNP 300
                                                                                                                                                                                           301 ILYVEMGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSI 350
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 18, Last annotation update)
0RPHAN SEVEN TRANSMEMBRANE RECEPTOR STRL33.
MACACA fascicularis (Crab eating macaque) (Cynomolgus monkey)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 DHYEDDGFLNSFNDSSQEE---HQDFLQFRKVFLPPCMYLVVFVCGLVGNSLVLVISIFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LACISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAIILLSIPQLVFYTV--NDNAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 AA; 39472 MW; 0961328F948E7784 CRC64;
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33.1%; Pred. No. 2.7e-42;
ive 73; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 AA,
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Best Local Similarity 33.1%
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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NCBI_TaxID=9541;
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SEQUENCE 343 AA; 394'
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MEDLINE-97311099; PubMed-9166430;
Liao F., Alkhattb G., Peden K.W., Sharma G., Berger E.A., Farber J.M.;
"STR133, A novel chemokine receptor-11ke protein, functions as a
fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-
                                                                                                                                                                                                                                                                                  An P., Winkler C., O'Brien S.J.;
"The Influence of a STRL33 mutant on the course of HIV-1 infection.";
"The Influence of a STRL33 mutant on the course of HIV-1 infection.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF029759; AF021918.1.
Interpro; IPR000276; GPCR_Rhodpsn.
PFfam; PR0001; 7tm_1.1.
PRINTS; PR00021; 7tm_1.1.
PROSITE; PS00237; GPCRRHODDPSN.
PROSITE; PS00237; GPROTEIN_RECEP_FI_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 LQSLTDVFLVNLPLADLVFVCTLPFWAYAGIHEWVFGQVMCKSLLGIYINFYTSMLILT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPQLVFYTV--NDNARCI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 QRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLA 131
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STRAIN=STRL33(BONZO);
Brussel A., Pretet J.L., Girard M., Butor C.;
Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and gpr15 (BOB).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 YHEDYGFSSFNDSSQEE----HQDFLQFSKVFLPCMYLVVFVCGLVGNSLVLVISIFYHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 VIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 PIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTV
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
G PROTEIN-COUPLED RECEPTOR STRL33.
Pan troglodytes (Chimpanzee).
Eukaaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherta; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 MGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 VSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSK--TFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 AA; 39279 MW; CE149633D01D20AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.8%; Score 560; DB 4; L
33.1%; Pred. No. 9.3e-42;
iive 75; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342
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EMBL; AF084229; AAD52041.1; -.
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                                                                                                                                                                                                           Exp. Med. 185:2015-2023(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | ||::||:: | || :: | | || 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 YIFYQKLRILIDVFLLNLPLADLVFVCTLPFWAYAGTYFWVFGTVMCKTLRGMYIMNFYV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 ILYVFMGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYYYEEN--EMNGTYDYSQYELICIKEDVR--EFAKVFLPVFLTIVFVIGLAGNSMVVAI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 DGHYEGDFWLFNNSSDNSQ-----ENKRFLKFKEVFLPCVYLVVFVFGLLGNSLVLII 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sato H., Taniguchi M.;

"Molecular cloning of a putative chemokine receptor preferentially expressed in mouse lymphocytes.";

expressed in mouse lymphocytes.";

submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF305709; AAG31284.1;

MGD; MGI:194582; Cxcr6.

InterPro; IPR000275; GFCR.Rhodpsn.

PRINTS; PR000377; GFCR.Rhodpsn.

PROSITE; PS002377; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.9%; Score 561.5; DB 11; Length 351; Best Local Similarity 35.4%; Pred. No. 7e-42; Matches 127; Conservative 69; Mismatches 126; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 AA; 40511 MW; B00E3134D2B4D1ED CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MUTANT G PROTEIN-COUPLED RECEPTOR STRL33.
                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                            351 AA
                                                                                                                              Created)
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                                                                            PRT;
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STRAIN-C57BL/6; TISSUE-SPLEEN;
                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19, PUTATIVE CHEMOKINE RECEPTOR
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                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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Q9HCA5;
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Matches 125;
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SEQUENCE
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MEDLINE-20368347; PubMed-10906389;
Alabyew Er., Najakshin A.M., Mechetina L.V., Taranin A.V.;
Alabyew Er., Najakshin a.M., Mechetina L.V., Taranin A.V.;
Alabyew Er., Najakshin a.M., Mechetina L.V., Taranin A.V.;
T.C. Incloning of a CXCR4 homolog in chondrostean fish and characterization of the CXCR4-specific structural features.";
T. C. Incloning of a CXCR4 homolog in chondrostean fish and characterization at the CXCR4-specific structural features.";
T. C. Incloning of a CXCR4 homolog in chondros.
T. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
T. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
T. SUBL: ALAG4488; CABG025.1;
T. DR FRAN; PRO001; 7tm_1; 1.
DR PRINTS; PRO0023; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PSO0226; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PSSO0262; G_PROTEIN_RECEP_F1_2; 1.
SROUENCE 358 AA; 40448 MW; 7B3B99B962453008 CRC64;
                                                                                                                                                                                                                                                                                                            132 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWNAAILLSIPQLVFYTV--NDNARCI 185
                                                                                                                                                                                                                                                                                                                                   72 QRTKTDVYILNLAVADLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLA 131
                                                                                                                                                                                                                                                                       6 YHEDYGFNSFNDSSQEE----HQDFLQFSKVFLPCMYLVVFVCGLVGNSLVLVISIFYHK 61
                                                                                                                                                                     Gaps
                                                                                                                                                                                           12 YYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKK 71
                                                                                                                                                                                                                                                                                                                                                                         186 PIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                  246 VIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GYHDEAISTVVLATQMTLGFFLPLLTMIVCYSVIIKTLLHAGGFQKHRSLKIIFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Chondrostei, Acipenseriformes, Acipenseridae,
Acipenserinae, Acipenser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 VSLKFRKNFWKLVKDIGCLPYLGVSHQWKSSEDNSK--TFSASHNVEATSMFQL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 MGASFKNYVMKVAKKYG-----SWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                                                                                                                                                  32;
                                                                                                                                      Length 342;
                                                                                                                                  30.7%; Score 559; DB 6; Length 34
33.1%; Pred. No. 1.1e-41;
Live 74; Mismatches 131; Indels
                                                                                        5B58003797806B2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
             Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
InterPro; IPR000276; GPCR_Rhodpsn
                                                                                         342 AA; 39273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acipenser ruthenus (sterlet).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                   Query Match 30.7%
Best Local Similarity 33.1%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHEMOKINE RECEPTOR 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7906;
                                                                          Receptor.
SEQUENCE
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   SO WW WW SO WW
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Length 358;

Score 544; DB 13; Pred. No. 2.6e-40;

29.9%;

Query Match Best Local Similarity

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9
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                                                                                                                                                                        127 MQFLACISIDRYVAVTKVPSQSGVGKPC-----WIICFCVWMAAILLSIPQLVFYTVNDN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-C CHEMOKINE RECEPTOR 4.

Rattus norvegious (Rat).

Eukaryota; Metazoa; Chondata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                           7 TVDFTFENNTEGSGSGDYSQYDEVCKRNLNGDLRKIFLPTVYTIIFVMGIVGNGLVVIVM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=LEW;
Garcia G.E., Chen S., Xia Y., Harrison J., Wilson C.B., Johnson R.J.,
Bacon K.B., Feng L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 VAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVSGMQFLACISIDRYVAVTKV-----PSQSGVGKPCWIICFCVWMAAILLSIPQLVF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 YTV---NDNARCIPIFPRYLGTSMKALIQMLEI-CIGFVVPFLIMGVCYFITARTLMKMP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 STDYYYEEN-EMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIY 66
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                                                                                                                                              67 AYYKKQRTKTDVYILNLAVADLLLETLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSG
                                                                                                                                                                                                                                                                          238 PLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 ALKTIILILAFFICWLPYCIAILVDTLVLLNVIQYNCTLQHHMETWIFVTEGLAYFHCC
                                                                                                                                                                                                                                                                                                                                             182 A---RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMK-MPNIKISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FYSGIFFIMLMSIDRYLAIVHAVFSLRARTLTYGV----ITSLITWSVAVFASLPGLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 LNPILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFS 349
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF432872; AAL30398.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 AA; 41218 MW; 5095C6CD299E1F8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
64; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Mismatches 127;
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Conservative
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Matches 113; Conservative
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Search completed: August
Job time: 143 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 YSGIFFISCMSLDKYLEIVHAQPYHRLRTRAKS-----LLLATIVWAVSLAVSIPDM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 MPNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTE 289
              124 VSGMQFLACISIDRYVAV-----TKVPSQSGVGKPCWIICFCVWMAAILLSIPQL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 VFYTVNDNAR----CIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 AIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNF 123
NIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENSSEYY-----YDYLDEVAFMLCRKDAVVSFGKVFLPVFYSLIFVLGLSGNLLLL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 LRPAGQGRALKIAAALVVAFFVLWFPYNLTLFLHTL-LDLQVFGNCEVSQHLDYALQVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOSTDYYYEENEMNGTYDYSQYE--LICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVV
                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UNKNOWN (FROTEIN FOR MGC:10475) (PROTEIN FOR MGC:10537).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.0%; Score 527; DB 4; Length 384
32.9%; Pred. No. 8.8e-39;
.ive 72; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                           Straugherg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011631; AAH11631.1; -.
EMBL; BC008816; AAH08816.1; -.
SFOURENCE 384 AA; 43442 MW; 464C5703C1DE9A6A CRC64;
                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                             384 AA.
                                                                                                                                                                                                                                                                                                    TISSUE-PLACENTA, AND CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                 TISSUE-PLACENTA, AND CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                  293 AFIHCCLNPVIYFFLGEKFRKYIAQL 318
                                                  292 ALFHSCLNPILYVFMGASFKNYVMKV 317
                                                                                                                                             PRT;
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09YGC3;
01-MAY-1999 (TrEMBLrel. 10, Cx
01-MAY-1999 (TrEMBLrel. 10, La
01-JUN-2001 (TrEMBLrel. 17, Le
CHEMOKINE RECEPTOR 4.
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Best Local Similarity 32.9
Matches 107; Conservative
                                                                                                                                             PRELIMINARY;
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                                                                                                                                                       Q96A02;
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Q9YGC3
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Q96A02
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79 YILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLACISIDRY 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAVTKVPSQSGVGKPC--WIICFCVWMAAILLSIPQLVFYTVND-NAR--CIPIFPRYLG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 NGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKKQRTKTDV 78
                                                                                                                                                                                    Moepps B., Knoepfle K., Brown M., Knoechel W., Glerschik P.;
"Expression of the CXC chemokine receptor 4 during early Xenopus
lacvis embryogenesis: a possible role of chemokine receptors as
regulators of development and differentiation.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPPORS.
EMBL; X17895; CAA76924.1;
-- EMBL; X17895; CAA76924.1;
-- InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETWTVGFRFLHITVGLILPGLIILICXCVIISKLSHSKGHQKRKALKTTVILILAFFACW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 TSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLTVVIVFIVTQ
                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.6%; Score 520.5; DB 13; Length 358; 35.9%; Pred. No. 3.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Mismatches 121;
laevis (African clawed frog).
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                                                                             Xenopodinae; Xenopus.
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Matches 108; Conserv
                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                            NCBI_TaxID=8355
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Search time 17.74 Seconds (without alignments) 1895.787 Million cell updates/sec
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4.5
Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2000
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                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1819
                                                                                           August
                                                                                                                                                      Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                      Scoring table:
                                                            OM protein
                                                                                                                                                                                                                                                                    Searched:
                                                                                           Run on:
```

283138

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

G protein-coupled lymphocyte specifi g protein-coupled G protein-coupled chemokine (G-C) re interleukin-8 rece probable G protein-cochambia G protein-coupled interleukin-8 rece interleukin-8 rece interleukin-8 rece neuropeptide Y/pep fusin (LESTRA) - C chemokine (G-C) re interleukin-8 rece interleukin-8 rece neuropeptide Y/pep fusin (LESTRA) - C chemokine (C-C) re interleukin-8 rece G protein-coupled macrophage inflamm chemokine (G-C) re chemokine (G-C) re chemokine (G-C) re chemokine (C-C) re rece G protein-coupled chemokine (C-C) re chemokine (C-C) re chemokine (C-C) re interleukin-8 rece MIP-1 alpha recept interferon-inducib interleukin-8 Description SUMMARIES JN0621 BB55735 A45680 JC5068 A57160 A57160 JC4580 JC4580 JC4580 JC4580 JC4580 JC4580 JC4580 JC4580 JC4580 JC2680 A57160 JC5068 A57160 A5716 A43113 A48921 I38450 I49341 JE0349 A45177 S42096 S55594 JC5067 I49339 Query Match Length DB 484.5 483.5 482 479.5 476.5 Score Result 

angiotensin II rec angiotensin II rec angiotensin II rec	II oupl	MIP-1 alpha recept G protein-coupled G protein-coupled	angiotensin II rec angiotensin II rec angiotensin II rec	G protein-coupled MDCR15 protein - h anglotensin II rec anglotensin II rec
S44425 JC1104 JC2134	S15403 S32785 A48857	149340 \$26667 \$42628	JN0694 A42656 JH0621	A39714 S56162 JQ1516 I39418
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359 359 359	359 374 359	356 372 374	362 359	362 327 359 359
25.0 24.9 24.9	24.7 24.7 24.5	24.5 24.3 24.3	24.2	24.1 24.1 23.9 23.6
455.5 452.5 452.5	450 450 446.5	445.5 442.5 42.5	441 439 438.5	438.5 437.5 434 428.5
30 31 32	34 35	36 38	36 4 4 0 1 1 0	44 44 45

## ALIGNMENTS

THE SECULT 1  C. DATE: 2.4-Teb-1994 Sequence_revision 24-Feb-1994 #text_change 19-May-2000  C. Accession: NB0621 : MOST, 7: AoK1, 3: Sato, T: Kutihara, K.  HIGHORIS TOWN Res. Commun. 134, Sato, T: Kutihara, K.  HIGHORIS TOWN Res. Commun. 134, Sato, T: Kutihara, K.  HIGHORIS TOWN Res. Commun. 134, Sato, T: Kutihara, K.  A. TILLE Identification of novel members of G-protein coupled receptor superfamily ex.  A. TILLE Identification of novel members of G-protein coupled receptor superfamily ex.  A. Restance annabar. 19621: MUID: 93326166  A. MOST Res. Commun. 134, Sato, 133, Sato, 134, S
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G protein-coupled receptor EBII - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: A55735
B; Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T Genomics 23, 643-650, 1994
A; Title: Cloning of human and mouse EBII, a lymphoid-specific G-protein-coupled recep A; Reference number: A55735; MUID:95154835
A; Accession: A55735
A; Accession: A55735
A; Status: proliminary
A; Mesidues: 1-378 cSCH-A;
A; Residues: 1-378 cSCH-A;
A; Residues: 1-378 cSCH-A;
A; Residues: 1-378 cSCH-A;
A; Cross-references: GB:L31580; NID:9468340; PIDN:AAA74232.1; PID:9468341
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
A45680
G protein-coupled peptide receptor EBI'l - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A65680
R:Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr Virus-induced genes: first lymphocyte-specific G protein-couple
A:Reference number: A45680; MUID:93188173
A:Accession: A45680
A:Accession: A45680; MUID:93188173
A:Accession: A45680
A:Accession: A45680
A:Accession: A45680
A:Accession: Breathinary
A:Molecule type: nucleic acid
A:Residues: 1:378 cBIR>
A:Cross-references: GBI-VBIPOCYtes
A:Cross-references: GB-IVMPhocytes
A:Cross-references: GB-IVMPhocytes
A:Cross-references: GB-IVMPhocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIP:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IALFHSCLNPILYVFMGASFKNYVMKVAKKYGSWRRQR------QSVEEFPFDSEGPTE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTES
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llarity 38.3%; Pred. No. 2.7e-48;
Conservative 67; Mismatches 125;
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No. 1.1e-47;
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Best Local Similarity
Matches 140; Conserv
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Best Local
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R.S. Burgetahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
Submitted to the EMBL Data Library, February 1995
A.Description: The expression of the chemokine receptor BLR2/EB11 is specifically transa A.Reference number: $52443
A.Accession: $55443
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (man)
                                                                                                                                                                                                                                                                        lymphocyte-specific G protein-coupled receptor EB11 - human
N.Alternate names: Burkltt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
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301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
                                        Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 2;
4.5e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: DNA
A.Rolecule type: DNA
A.Cross-references: EMBL:X84702
Genetics:
A.Gene: GDB:CMKBR7; EB11; BLR2; CCR7
A.Cross-references: GDB:342065; OMIM:600242
A.Map Postition: 17q12-17q11. 2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 659;
Pred. No. 4
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38.7%; Pre
tive 66;
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Best Local Similarity 38.78
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEGPTEPTSTFS 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-378 <SCH>
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A; Gene: C125.
A; Map position: 3p21-3p21
C; Superfamily: vertebrate rhodopsin
F; 40-65/Domain: transmembrane #status predicted <TM3>
F; 112-137/Domain: transmembrane #status predicted <TM3>
F; 121-137/Domain: transmembrane #status predicted <TM4>
F; 201-206/Domain: transmembrane #status predicted <TM5>
F; 201-306/Domain: transmembrane #status predicted <TM6>
F; 201-306/Domain: transmembrane #status predicted <TM7>
F; 201-306/Domain: transmembrane #status predicted <TM6>
F; 201/Minding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicte
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R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor A;Reference number: A57160; MUID:95370289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 HKAIRVIIAVVLVFLACQIPHNMVLLVTAAN-LGKMNRSCQSEKLIGYTKTVTEVLAFLH 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SERIAL STATEMENT STATEMENT
           MQFLACISIDRYVAVTKVPS----QSGVGKPCWIICFCVWMAAILLSIPQLVF---YTVN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 VMLMSIDRYLAIVHAVFSLRARTLIYGV ----ITSLAIWSVAVFASLPGFLFSTCYTER 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Note: source clone K5-5
C;Genetics:
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                                                                                                                                                                                                                                                                                         GSDVC---EPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFMIFCYTFIVKTLVQAQNSKR
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                                                                                       MLLLTCISMDRYIAIVQATKSFRLFSRTLPRSKIICLVVWGLSVIISSSTFVFNQKYNTQ
                                                                                                                                                                                                                              DNARCIPIFPRYLGTS----MKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 SRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 DYYYEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVAIYAYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 CCLNPVLYAFIGQKFRNYFLKILKDLWCVRRYKS 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCLNPILYVFMGASFKNYVMKVAKKYGSWRRQRQS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemokine (C-C) receptor 4 -
N;Alternate names: C-C CKR-4
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G protein-coupled receptor CKR-L3 - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C; Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C; Date: 31-Jan-1997 #sequence_revision
R; Accession: Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
R; Zaballos, A: Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A; Title: Molecular cloning and RNA expression of two new human chemokine receptor-like
A; Reference number: JC5068
A; Accession: JC5068
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A.Residues: 1-369 < ZABA.
A.Residues: 1-369 = DNA
C.Comment: This protein belongs to the family of alpha chemokine receptors.
C.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Gene: GDB:5370639; OMIN:601835
A.Map position: 6427-6427
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate status predicted <TMJ>
F.42-68/Domain: transmembrane #status predicted <TMJ>
F.115-136/Domain: transmembrane #status predicted <TMJ>
F.115-136/Domain: transmembrane #status predicted <TMJ>
F.115-137/Domain: transmembrane #status predicted <TMJ>
F.115-137/Domain: transmembrane #status predicted <TMG>
F.250-771/Domain: transmembrane #status predicted <TMG
     8;
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C; Species: Rattus norvegicus (Norway rat)

C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C; Accession: 158186

R; Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A; Title: CDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord an A; Reference number: 158186; MUID:94323113
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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
                                                                               MKMPNIKISRPLKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQV 287
                                                                                                                                                                                                                                                                                                                                                                                                           orphan G protein-coupled receptor - human
N:Alternate names: V28 protein
C;Species: Homo sapiens (man)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Accession: JC4304
                              F----YTVNDNARCIPIFPRYLG---TSMKALIQMLEICIGFVVPFLIMGVCYFITARTL 227
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
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C; Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C; Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C; Accession: 137898; 138712; A53611; A39446
R; Ahula, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A; Title: Comparison of the genomic organization and promoter function for human interlet A; Accession: 137898
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A Status: preliminary
A Molecule type: DNA
A Molecule type: DNA
A Residues: 6-360 <SPR>
A Cross-references: GB:M99412; GB:L19593
B R.Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Across references: EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11873; I1876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878; NID:g511816; PID:g511819; EMBL:U11878; NID:g511816; PID:g511819; EMBL:U11878; NID:g511819; PID:g511819; EMBL:U11878; NID:g511810; Chem. 269, 11065-11072; 1994
A:Title: Structure, genomic organization, and expression of the human interleukin-8 recent Parameters of the human interleukin-8 recent Par
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A; Residues: 6-360 <MUR>
A; Residues: 6-360 <MUR>
A; Cross-references: GB:M73969
C; Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
C; Genetics:
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LKVLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCL 298
                                                                 241 VKMIFAVVVELGEWTPYNIVLFLETL-VELEVLQDCTFERYLDYAİQATETLAFVHCCL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule Fype: DNA A; Molecule Fype: MRNA A; Mo
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A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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A; Accession: A39446
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                                                                                                                                                              299 NPILYVFMGASFKNYVMKVAK 319
                                                                                                                                                                                                                       Conservative
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Best Local Simi
Matches 120;
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Length 360;

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F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted F;72,202,350/Banding site: phosphate (Ser) (covalent) (by casein kinase II) #status p:F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicte
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C;Species: Homo sapiens (man)
C;Date: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
C;Accession: B55733
R;Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui Genomics 23, 609-618, 1994
A;Title: Cloning of human genes encoding novel G protein-coupled receptors.
A;Reference number: A55733; MUID:95154831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 VAIYAYYKKQRTKTDVYILNLAVADLLLFFTLPFWAVNAVHGWVLGKIMCKITSALYTLN 122
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                                                                                                                                                                                                                                                                                                        69; Mismatches 128;
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A;Map position: 17421.1.17421.3
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-354 < MAR>
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Matches 110;
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Matches 121;
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A.Experimental source: pertpheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and A;Gene: v28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ដ
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C; Accession: JQ4587
R; Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A; Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines
A; Reference number: JQ4587; MUID:96136324
A; Molecule type: mRNA
                                                                                   related
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A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
                                                                       A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely A;Reference number: JC4304; MUID:96011651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLACISIDRYVAV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 NLALSDLLFVATLPFWTHYLINEKGLHNAMCKFTTAFFFIGFFGSIFFITVISIDRYLAI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 TKVPS-----QSGVGKPCWIICFCVWMAAILLSIPQLVFYTVNDNARCIPIFPRYLGT 194
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Gene 163, 295-299, 1995
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C;Keywords: 91ycoprotein; phosphoprotein; receptor; thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superfamily: vertebrate rhodopsin
C; Superdeal: G protein-coupled receptor; lymphokine; tran
E; 35-57/Domain: transmembrane #status predicted <TM1>
E; 66-88/Domain: transmembrane #status predicted <TM2>
E; 104-125/Domain: transmembrane #status predicted <TM3>
E; 105-100main: transmembrane #status predicted <TM3>
E; 107-217/Domain: transmembrane #status predicted <TM5>
E; 230-254/Domain: transmembrane #status predicted <TM5>
E; 275-296/Domain: transmembrane #status predicted <TM6>
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                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-355 <RAP>
                                                                                                                                                      A; Accession: JC4304
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A; Molecule type: DNA
A; Residues: 1-355 <BEC>
A; Residues: 1-355 <BEC>
A; Cross references: GBEM74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
B; Lee, J; Kuang, W.J; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A; Tille: Characterization of complementary DNA clones encoding the rabbit IL-8 recept
A; Reference number: A46483; MUID:92148149
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Dete: 31-Mar-1992 #sequence_revision 31-Mar-1992 #sext_change 05-Nov-1999
C;Accession: JQ1231; A46483
B;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyma
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A;Title: Molecular characterization of the interleukin-8 receptor.
A;Reference number: JQ1231; MUID:91378994
                             CIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLL 243
                                                                                        244 TVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILY 303
                                                                                                                                                                                                                                                                         GNSMVVAIYAYYKKQRTKTDVYILNLAVADLLLLFTLPFWAVNAVHGWVLGKIMCKITSA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 358;
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Best Local Similarity
Matches 116; Conserva
                             184
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N.Alternate names: fusin; HM89; leukocyte-derlved seven-transmembrane receptor LESTR; C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo Hardo, I.G.; Duncan, A.W.)
C.Species: Homo Hardo, I.G.; Duncan, A.M.
C.Species: Homo Hardo, Hardo, I.G.; Duncan, A.M.
C.Species: Homo Hardo, Hardo, Hardo, Hardo, Hardo, Hardon, A.M.
C.Species: Homo Hardo, Hardo, Hardon, Hardon
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A.Residues: 1-352 <LOE>
A.Cross-references: BMBL:X71635; NID:9297099; PIDN:CAA50641.1; PID:9297100
BY.Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A;Title: Molecular cloning, characterization, and localization of the human homolog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Experimental source: neutrophils
A;Experimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C;Superfamily: vertebrate rhodopsin
C;Superfamily: optein-coupled receptor; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 355;
                                                                                                                                                                                                                                                                                                  Superfamily: vertebrate rhodopsin
Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.6%; Score 501.5; DB 2; 33.1%; Pred. No. 1.4e-35; tive 70; Mismatches 127;
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Best Local Similarity
Matches 107; Conserv
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Search completed: August
Job time: 192 sec
  A; Residues: 1-353 <RIM>
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                                       A:Status: preliminary: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Molecule type: 1352 cHER>
A:Cross-references: GB:L06797; NID:9414929; PIDN:AAA03209.1; PID:9414928
R:Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; Lax
R:Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; Lax
A;Title: A proposed bovine neuropeptide Y (NPY) receptor CDNA clone, or its human homolo
                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mSNA
A;Cross-references: GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314
B;Nomura, H.; Nielsen, B.W.; Matsushima, K.
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem A;Reference number: 154751; MUID:94092629
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C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
C; Accession: S28787
Mol. Pharmacol. 40, 869-875, 1991
A.Title: Sequence and expression of a neuropeptide Y receptor CDNA.
A.Reference number: S28787; MUID: 92100053
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 RCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :| | : | | : | | :| 185 ICDRFYPNDLWV---VVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTT 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 QFLACISIDRYVAVTKVPSQSGVGKPC--WIICFCVWMAAILLSIPQLVFYTV---NDNA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :::: | ||| || ::: | : | | |||||| || 242 VILILAFFACWLPYXIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPIL 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 LTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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A;Map position: 2421-2421
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 27.5%; Score 500.5; DB 2; Best Local Similarity 34.6%; Pred. No. 1.7e-35; Matches 107; Conservative 57; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: 169203
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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A; Reference number: I53006; MUID: 93319629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: NPY3R; NPYY3
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YAFLGAKFK 310
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RTKTDVYILNLAVADLLLFTLPFWAVNAVHGWVLGKIMCKITSALYTLNFVSGMQFLAC 132
                                                                                                                                                                                                                                                                                                     185 IPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLKVLLT 244
                                                                                                                                                                                                                                                                                                                                                                 133 ISIDRYVAVTKVPSQSGVGKPC----WIICFCVWMAAILLSIPQLVF---YTVNDNARC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVIVFIVTQLPYNIVKFCRAIDIIYSLITSCNMSKRMDIAIQVTESIALFHSCLNPILYV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                      13 YEENEMNGTYDYSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVVAIYAYYKKQ 72
A;Cross-references: EMBL:M86739
C;Superfamily: vertebrate rhodopsin
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                             Length 353;
                                                                                                                                                  Indels
                                                                                                         27.5%; Score 499.5; DB 2; 34.5%; Pred. No. 2.1e-35; iive 60; Mismatches 126;
                                                                                                           Query Match
Best Local Similarity 34.5%
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|| ||
FLGAKFK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 FMGASFK 311
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